

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/567,403 A
Source: IFWO
Date Processed by STIC: 07/05/2006

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RAW SEQUENCE LISTING

DATE: 07/05/2006

PATENT APPLICATION: US/10/567,403A

TIME: 08:18:48

Input Set : A:\8830-390US1.txt

Output Set: N:\CRF4\07052006\J567403A.raw

3 <110> APPLICANT: CSS- Albachem Limited
4 Cotton, Graham
6 <120> TITLE OF INVENTION: Ligation Method
8 <130> FILE REFERENCE: 08830-0390US1 (47596-221330)
10 <140> CURRENT APPLICATION NUMBER: US 10/567,403A
11 <141> CURRENT FILING DATE: 2006-02-03
13 <150> PRIOR APPLICATION NUMBER: GB 0318276.3
14 <151> PRIOR FILING DATE: 2003-08-05
16 <150> PRIOR APPLICATION NUMBER: GB 0320122.5
17 <151> PRIOR FILING DATE: 2003-08-28
19 <160> NUMBER OF SEQ ID NOS: 6
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 27
25 <212> TYPE: PRT
26 <213> ORGANISM: Artificial sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Synthetic C-terminal thioester peptide
32 <220> FEATURE:
33 <221> NAME/KEY: misc_feature
34 <222> LOCATION: (1)..(1)
35 <223> OTHER INFORMATION: Xaa may be alanine or arginine
37 <220> FEATURE:
38 <221> NAME/KEY: misc_feature
39 <222> LOCATION: (7)..(7)
40 <223> OTHER INFORMATION: Xaa may be alanine or arginine
42 <220> FEATURE:
43 <221> NAME/KEY: misc_feature
44 <222> LOCATION: (9)..(9)
45 <223> OTHER INFORMATION: (Me)3
47 <220> FEATURE:
48 <221> NAME/KEY: misc_feature
49 <222> LOCATION: (15)..(15)
50 <223> OTHER INFORMATION: Xaa may be alanine or arginine
52 <220> FEATURE:
53 <221> NAME/KEY: misc_feature
54 <222> LOCATION: (21)..(21)
55 <223> OTHER INFORMATION: Xaa may be alanine or arginine
57 <220> FEATURE:
58 <221> NAME/KEY: misc_feature
59 <222> LOCATION: (24)..(24)
60 <223> OTHER INFORMATION: Xaa may be alanine or arginine
62 <220> FEATURE:

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63 <221> NAME/KEY: misc_feature
64 <222> LOCATION: (25)..(25)
65 <223> OTHER INFORMATION: Xaa may be alanine or arginine
67 <400> SEQUENCE: 1
W--> 69 Xaa Arg Thr Lys Gln Thr Xaa Arg Lys Ser Thr Gly Gly Lys Xaa Pro
70 1          5          10          15
73 Arg Lys Gln Leu Xaa Thr Lys Xaa Xaa Arg Lys
74          20          25
77 <210> SEQ ID NO: 2
78 <211> LENGTH: 102
79 <212> TYPE: PRT
80 <213> ORGANISM: Homo sapiens
82 <400> SEQUENCE: 2
84 His Pro Trp Phe Phe Gly Lys Ile Pro Arg Ala Lys Ala Glu Glu Met
85 1          5          10          15
88 Leu Ser Lys Gln Arg His Asp Gly Ala Phe Leu Ile Arg Glu Ser Glu
89          20          25          30
92 Ser Ala Pro Gly Asp Phe Ser Leu Ser Val Lys Phe Gly Asn Asp Val
93          35          40          45
96 Gln His Phe Lys Val Leu Arg Asp Gly Ala Gly Lys Tyr Phe Leu Trp
97          50          55          60
100 Val Val Lys Phe Asn Ser Leu Asn Glu Leu Val Asp Tyr His Arg Ser
101 65          70          75          80
104 Thr Ser Val Ser Arg Asn Gln Gln Ile Phe Leu Arg Asp Ile Glu Gln
105          85          90          95
108 Val Pro Gln Gln Pro Thr
109          100
112 <210> SEQ ID NO: 3
113 <211> LENGTH: 36
114 <212> TYPE: PRT
115 <213> ORGANISM: Artificial sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: Purified and lyophilised Grb2-SH2 C terminal hydrazide
treated
119          with protease Lys-C in 100mM ammonium bicarbonate buffer
121 <400> SEQUENCE: 3
123 Phe Asn Ser Leu Asn Glu Leu Val Asp Tyr His Arg Ser Thr Ser Val
124 1          5          10          15
127 Ser Arg Asn Gln Gln Ile Phe Leu Arg Asp Ile Glu Gln Val Pro Gln
128          20          25          30
131 Gln Pro Thr Gly
132          35
135 <210> SEQ ID NO: 4
136 <211> LENGTH: 392
137 <212> TYPE: PRT
138 <213> ORGANISM: Homo sapiens
140 <400> SEQUENCE: 4
142 Met Lys Ile Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys
143 1          5          10          15
146 Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr

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147          20          25          30
150 Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
151          35          40          45
154 Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
155          50          55          60
158 His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile
159 65          70          75          80
162 Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp
163          85          90          95
166 Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu
167          100         105         110
170 Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys
171          115         120         125
174 Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly
175          130         135         140
178 Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro
179 145         150         155         160
182 Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys
183          165         170         175
186 Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly
187          180         185         190
190 Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp
191          195         200         205
194 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala
195          210         215         220
198 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys
199 225         230         235         240
202 Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser
203          245         250         255
206 Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro
207          260         265         270
210 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp
211          275         280         285
214 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala
215          290         295         300
218 Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala
219 305         310         315         320
222 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln
223          325         330         335
226 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala
227          340         345         350
230 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn
231          355         360         365
234 Ser Ser Ser Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Leu Gly Ile
235          370         375         380
238 Glu Gly Arg Gly Thr Leu Glu Gly
239 385         390
242 <210> SEQ ID NO: 5
243 <211> LENGTH: 5

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244 <212> TYPE: PRT
245 <213> ORGANISM: Artificial sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Small synthetic C-terminal hydrazide peptide
250 <400> SEQUENCE: 5
252 Ser Leu Ala Tyr Gly
253 1 5
256 <210> SEQ ID NO: 6
257 <211> LENGTH: 11
258 <212> TYPE: PRT
259 <213> ORGANISM: Artificial sequence
261 <220> FEATURE:
262 <223> OTHER INFORMATION: Synthetic peptide corresponding to the c-myc epitope
sequence was
263 synthesised GEQKLISEED-NH2 whereby pyruvic acid was coupled to
264 the amino terminus of the peptide as the last step of the
265 assembly
268 <220> FEATURE:
269 <221> NAME/KEY: MOD_RES
270 <222> LOCATION: (11)..(11)
271 <223> OTHER INFORMATION: AMIDATION
273 <400> SEQUENCE: 6
275 Gly Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
276 1 5 10

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 1, 7, 15, 21, 24, 25

VERIFICATION SUMMARY

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L:69 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0

M:341 Repeated in SeqNo=1